



OIPE

6/11/02

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/828,574

DATE: 02/26/2002  
TIME: 11:09:41

Input Set : A:\UCSD1310-1.ST25.txt  
Output Set: N:\CRF3\02262002\I828574.raw

2 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
3 ALBANI, Salvatore  
4 PRAKKEN, Berent J.  
6 <120> TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF  
8 <130> FILE REFERENCE: UCSD1310-1  
10 <140> CURRENT APPLICATION NUMBER: US 09/828,574  
11 <141> CURRENT FILING DATE: 2001-04-06  
13 <150> PRIOR APPLICATION NUMBER: US 60/224,104  
14 <151> PRIOR FILING DATE: 2000-08-09  
16 <160> NUMBER OF SEQ ID NOS: 13  
18 <170> SOFTWARE: PatentIn version 3.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 573  
22 <212> TYPE: PRT  
23 <213> ORGANISM: Homo sapiens  
25 <400> SEQUENCE: 1

27 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg  
28 1 5 10 15  
31 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe  
32 20 25 30  
35 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
36 35 40 45  
39 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile  
40 50 55 60  
43 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val  
44 65 70 75 80  
47 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys  
48 85 90 95  
51 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly  
52 100 105 110  
55 Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe  
56 115 120 125  
59 Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val  
60 130 135 140  
63 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys  
64 145 150 155 160  
67 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala  
68 165 170 175  
71 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys  
72 180 185 190  
75 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn  
76 195 200 205  
79 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile

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80      210                215                220
83 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
84 225                230                235                240
87 Asp Ala Tyr Val Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
88                245                250                255
91 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
92                260                265                270
95 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
96                275                280                285
99 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
100      290                295                300
103 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
104 305                310                315                320
107 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
108                325                330                335
111 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
112                340                345                350
115 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
116                355                360                365
119 Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
120      370                375                380
123 Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
124 385                390                395                400
127 Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
128                405                410                415
131 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
132                420                425                430
135 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
136                435                440                445
139 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
140      450                455                460
143 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
144 465                470                475                480
147 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
148                485                490                495
151 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
152                500                505                510
155 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
156      515                520                525
159 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
160      530                535                540
163 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
164 545                550                555                560
167 Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
168                565                570
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 15
173 <212> TYPE: PRI
174 <213> ORGANISM: Mycobacterium

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176 <400> SEQUENCE: 2
178 Gly Glu Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr
179 1 5 10 15
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 15
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 3
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190 1 5 10 15
193 <210> SEQ ID NO: 4
194 <211> LENGTH: 15
195 <212> TYPE: PRT
196 <213> ORGANISM: Mycobacterium
198 <400> SEQUENCE: 4
200 Pro Tyr Ile Leu Leu Val Ser Ser Lys Val Ser Thr Val Lys Asp
201 1 5 10 15
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 15
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 5
211 Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
212 1 5 10 15
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 15
217 <212> TYPE: PRT
218 <213> ORGANISM: Mycobacterium
220 <400> SEQUENCE: 6
222 Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys
223 1 5 10 15
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 15
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapiens
231 <400> SEQUENCE: 7
233 Lys Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys
234 1 5 10 15
237 <210> SEQ ID NO: 8
238 <211> LENGTH: 15
239 <212> TYPE: PRT
240 <213> ORGANISM: Mycobacterium
242 <400> SEQUENCE: 8
244 Ile Ala Gly Leu Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys
245 1 5 10 15
248 <210> SEQ ID NO: 9
249 <211> LENGTH: 15
250 <212> TYPE: PRT
251 <213> ORGANISM: Homo sapiens

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253 <400> SEQUENCE: 9  
 255 Val Ala Ser Leu Leu Thr Thr Ala Glu Val Val Val Thr Glu Ile  
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 261 <212> TYPE: PRT  
 262 <213> ORGANISM: Artificial sequence  
 264 <220> FEATURE:  
 265 <223> OTHER INFORMATION: dnaJp1 peptide  
 267 <400> SEQUENCE: 10  
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 270 1 5 10 15  
 273 <210> SEQ ID NO: 11  
 274 <211> LENGTH: 15  
 275 <212> TYPE: PRT  
 276 <213> ORGANISM: Artificial sequence  
 278 <220> FEATURE:  
 279 <223> OTHER INFORMATION: Irrelevant dnaJpV peptide  
 281 <400> SEQUENCE: 11  
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 284 1 5 10 15  
 287 <210> SEQ ID NO: 12  
 288 <211> LENGTH: 11  
 289 <212> TYPE: PRT  
 290 <213> ORGANISM: Artificial sequence  
 292 <220> FEATURE:  
 293 <223> OTHER INFORMATION: pan-DR binder peptide  
 295 <220> FEATURE:  
 296 <221> NAME/KEY: MISC\_FEATURE  
 297 <222> LOCATION: (2)..(2)  
 298 <223> OTHER INFORMATION: Xaa is any amino acid  
 300 <400> SEQUENCE: 12  
 W--> 302 Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala  
 303 1 5 10  
 306 <210> SEQ ID NO: 13  
 307 <211> LENGTH: 573  
 308 <212> TYPE: PRT  
 309 <213> ORGANISM: Homo sapiens  
 311 <400> SEQUENCE: 13  
 313 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg  
 314 1 5 10 15  
 317 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe  
 318 20 25 30  
 321 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
 322 35 40 45  
 325 Asp Ala Val Ala Val Thr Met Glu Pro Lys Gly Arg Thr Val Ile Ile  
 326 50 55 60  
 329 Gln Gln Ser Trp Gly Ser Pro Asn Val Thr Lys Asp Gly Val Thr Val  
 330 65 70 75 80

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333 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
334      85      90      95
337 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ser Gly Asp Gly
338      100      105      110
341 Thr Thr Thr Ala Thr Val Leu Ala Glu Ser Ile Ala Lys Glu Gly Phe
342      115      120      125
345 Gln Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
346      130      135      140
349 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
350 145      150      155      160
353 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Met Ile Ser Ala
354      165      170      175
357 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
358      180      185      190
361 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
362      195      200      205
365 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
366      210      215      220
369 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
370 225      230      235      240
373 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Val Gln Ser
374      245      250      255
377 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His His Lys Pro Leu Val
378      260      265      270
381 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Ile Leu
382      275      280      285
385 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
386      290      295      300
389 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
390 305      310      315      320
393 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
394      325      330      335
397 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
398      340      345      350
401 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Leu Glu
402      355      360      365
405 Lys Arg Ile Gln Glu Ile Ile Gly Gln Leu Asp Val Thr Thr Ser Glu
406      370      375      380
409 Tyr Glu Lys Glu Lys Leu Asn Glu Trp Leu Ala Lys Leu Ser Asp Gly
410 385      390      395      400
413 Val Val Val Leu Lys Phe Gly Gly Thr Ser Asp Val Glu Val Asn Glu
414      405      410      415
417 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
418      420      425      430
421 Glu Gly Gly Ile Val Leu Gly Gly Gly Phe Ala Leu Leu Arg Cys Ile
422      435      440      445
425 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
426      450      455      460
429 Met Glu Ile Val Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Thr Ala

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VERIFICATION SUMMARY

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Input Set : A:\UCSD1310-1.ST25.txt

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L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12